

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/734,692A
Source: EFW/b
Date Processed by STIC: 4/27/07

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 04/27/2007

PATENT APPLICATION: US/10/734,692A

TIME: 11:11:24

Input Set : A:\FORS 003 Subsitute US Seq.txt

Output Set: N:\CRF4\04272007\J734692A.raw

3 <110> APPLICANT: Stashenko, Philip
 4 Okamatsu, Yoshimura
 5 Sasaki, Hajime
 6 Battaglino, Richard
 7 Spaete, Ulrike
 9 <120> TITLE OF INVENTION: Expressed Genes that Define the Osteoclast Phenotype
 11 <130> FILE REFERENCE: 25669-003
 13 <140> CURRENT APPLICATION NUMBER: 10/734,692A
 14 <141> CURRENT FILING DATE: 2003-12-11
 16 <150> PRIOR APPLICATION NUMBER: 60/432,700
 17 <151> PRIOR FILING DATE: 2002-12-11
 19 <160> NUMBER OF SEQ ID NOS: 50
 21 <170> SOFTWARE: PatentIn version 3.2
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 22
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Mus musculus
 28 <400> SEQUENCE: 1
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 32 <210> SEQ ID NO: 2
 33 <211> LENGTH: 23
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Mus musculus
 37 <400> SEQUENCE: 2
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 42 <211> LENGTH: 1118
 43 <212> TYPE: DNA
 44 <213> ORGANISM: Mus musculus
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 51 agtccagagc agtctgaagg cacagcaagg gcttgaaatt gaaatgtttc acatgggctt 180
 53 tcaagactct tcagattgct gcctgtccta taactcacgg attcagtgtt caagatttat 240
 55 aggttatttt cccaccagtg gtgggtgtac caggccgggc atcatcttta tcagcaagag 300
 57 ggggttccag gtctgtgcc accccagtg tgggagagtt cagagatgca ttgaaagatt 360
 59 ggagaaaaac tcacaaccac ggacctacaa acaataacat ttgctttaga gaaggggtgtg 420
 61 aactgccagc tactttcttt ggtcttcccc agtgaccacc taagtggctc taagtgttta 480
 63 tttttatagg tatataaaca tttttttttt ctgtttccac tttaaagtgg catatctggc 540
 65 tttgtcacag aggggaaact tgtctgtgcc aacccagtc atctgaaaac tcagatgcct 600
 67 gggaaggtct gaagctgacc tcaatgacta cacataatat ttgattgaga taaatgggca 660
 69 aggtctggag agatggcttg gtgggttaaga gcacctgctg ctcttccaga ggacctgggt 720
 71 tcaattccca cttagatggc agctcaaact atctataatt ccaattccaa agaaaactga 780

(ps.6)

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73 tgccctatttt tgccccttta gttagtagta tttacagtat tctttataaaa ttcaccttga      840
75 catgaccatc ttgagctaca gccatcctaa ctgcctcaga atcactcaag ttcttccact      900
77 cgggtttccca gcggtatttta agtggataaaa ctgtgagagt ggtctgtggg acttttgaat      960
79 gtgtctgggtt ctgatagtca cttatggcaa cccaggtaca ttcaactagg atgaaataaa    1020
81 ttctgcctta gccagtagt atgtctgtgt ttgtaaggac ccagctgatt ttcccaccac    1080
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87 <211> LENGTH: 122

88 <212> TYPE: PRT

89 <213> ORGANISM: Mus musculus

91 <400> SEQUENCE: 4

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97 Leu Gly Ile Trp Ala Gln Ile Thr His Ala Thr Glu Thr Lys Glu Val
98          20          25          30
101 Gln Ser Ser Leu Lys Ala Gln Gln Gly Leu Glu Ile Glu Met Phe His
102          35          40          45
105 Met Gly Phe Gln Asp Ser Ser Asp Cys Cys Leu Ser Tyr Asn Ser Arg
106          50          55          60
109 Ile Gln Cys Ser Arg Phe Ile Gly Tyr Phe Pro Thr Ser Gly Gly Cys
110 65          70          75          80
113 Thr Arg Pro Gly Ile Ile Phe Ile Ser Lys Arg Gly Phe Gln Val Cys
114          85          90          95
117 Ala Asn Pro Ser Asp Arg Arg Val Gln Arg Cys Ile Glu Arg Leu Glu
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121 Lys Asn Ser Gln Pro Arg Thr Tyr Lys Gln
122          115          120

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126 <211> LENGTH: 2156

127 <212> TYPE: DNA

128 <213> ORGANISM: Homo sapiens

130 <400> SEQUENCE: 5

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135 atgcaactcc gtgccagaag gtgaacgaga gggcctttgg ggcccaactg ctgccccctc      180
137 tgtactcctt ggtatttgtc attggcctgg ttggaaacat cctggtggtc ctggtccttg      240
139 tgcaatacaa gaggctaaaa aacatgacca gcatctacct cctgaacctg gccatttctg      300
141 acctgctctt cctgttcacg cttcccttct ggatcgacta caagttgaag gatgactggg      360
143 tttttggtga tgccatgtgt aagatcctct ctgggtttta ttacacaggc ttgtacagcg      420
145 agatcttttt catcatcctg ctgacgattg acaggtacct ggccatcgtc cagcccggtg      480
147 ttgccttgcg ggcacggacc gtcacttttg gtgtcatcac cagcatcatc atttgggcc      540
149 tggccatctt ggcttccatg ccaggcttat acttttccaa gacccaatgg gaattcactc      600
151 accacacctg cagccttcac tttcctcacg aaagcctacg agagtggaag ctgtttcagg      660
153 ctctgaaact gaacctcttt gggctgggat tgcctttgtt ggtcatgac atctgctaca      720
155 cagggattat aaagattctg ctaagacgac caaatgagaa gaaatccaaa gctgtccggt      780
157 tgatttttgt catcatgac atcttttttc tcttttggac cccctacaat ttgactatac      840
159 ttatttctgt tttccaagac ttctgttca cccatgagtg tgagcagagc agacatttgg      900
161 acctggctgt gcaagtgacg gaggtgatcg cctacacgca ctgctgtgtc aaccagtg      960
163 tctacgcctt cgttggtgag aggttccgga agtacctgcg gcagttgttc cacaggcg      1020

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165 tggctgtgca cctgggttaaa tggctcccct tcctctccgt ggacaggctg gagagggtca 1080
167 gctccacatc tccctccaca ggggagcatg aactctctgc tgggttctga ctcagaccat 1140
169 aggaggccaa cccaaaataa gcaggcgtga cctgccaggc acactgagcc agcagcctgg 1200
171 ctctcccagc caggttctga ctcttggcac agcatggagt cacagccact tgggatagag 1260
173 agggaatgta atgggtggcct ggggcttctg aggcttctgg ggcttcagtc ttttccatga 1320
175 acttctcccc tggtagaaag aagatgaatg agcaaaacca aatattccag agactgggac 1380
177 taagtgtacc agagaagggc ttggactcaa gcaagatttc agatttgtga ccattagcat 1440
179 ttgtcaacaa agtcaccacac ttcccactat tgcttgacac aaccaattaa acccagtagt 1500
181 ggtgactgtg ggctccattc aaagtgagct cctaagccat gggagacact gatgtatgag 1560
183 gaatttctgt tcttccatca cctccccccc cccgccaccc tcccactgcc aagaacttgg 1620
185 aaatagtgat ttccacagtg actccactct gagtcccaga gccaatcagt agccagcatc 1680
187 tgcctcccct tcaactccac cgcaggattt gggctcttgg aatcctgggg aacatagaac 1740
189 tcatgacgga agagttgaga cctaacgaga aatagaaatg ggggaactac tgctggcagt 1800
191 ggaactaaga aagcccttag gaagaatttt tatatccact aaaatcaaac aattcaggga 1860
193 gtgggctaag cacgggccat atgaataaca tgggtgtgctt cttaaaatag ccataaaggg 1920
195 gagggactca tcatttccat ttacccttct tttctgacta tttttcagaa tctctcttct 1980
197 tttcaagttg ggtgatatgt tggtagattc taatggcttt attgcagcga ttaataacag 2040
199 gcaaaaggaa gcagggttgg tttcccttct ttttgttctt catctaagcc ttctggtttt 2100
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204 <210> SEQ ID NO: 6

205 <211> LENGTH: 355

206 <212> TYPE: PRT

207 <213> ORGANISM: Homo sapiens

209 <400> SEQUENCE: 6

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215 Asp Tyr Gly Asp Ala Thr Pro Cys Gln Lys Val Asn Glu Arg Ala Phe
216 20 25 30
219 Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Val Ile Gly
220 35 40 45
223 Leu Val Gly Asn Ile Leu Val Val Leu Val Leu Val Gln Tyr Lys Arg
224 50 55 60
227 Leu Lys Asn Met Thr Ser Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
228 65 70 75 80
231 Leu Leu Phe Leu Phe Thr Leu Pro Phe Trp Ile Asp Tyr Lys Leu Lys
232 85 90 95
235 Asp Asp Trp Val Phe Gly Asp Ala Met Cys Lys Ile Leu Ser Gly Phe
236 100 105 110
239 Tyr Tyr Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
240 115 120 125
243 Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala
244 130 135 140
247 Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Ile Ile Trp Ala Leu
248 145 150 155 160
251 Ala Ile Leu Ala Ser Met Pro Gly Leu Tyr Phe Ser Lys Thr Gln Trp
252 165 170 175
255 Glu Phe Thr His His Thr Cys Ser Leu His Phe Pro His Glu Ser Leu
256 180 185 190
259 Arg Glu Trp Lys Leu Phe Gln Ala Leu Lys Leu Asn Leu Phe Gly Leu

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263 Val	Leu Pro	Leu Leu Val	Met Ile Ile Cys Tyr Thr Gly Ile Ile Lys
264	210	215	220
267 Ile	Leu Leu Arg Arg	Pro Asn Glu Lys Lys Ser	Lys Ala Val Arg Leu
268 225		230	235 240
271 Ile	Phe Val Ile Met Ile Ile Phe Phe	Leu Phe Trp Thr Pro Tyr Asn	
272	245	250	255
275 Leu	Thr Ile Leu Ile Ser Val Phe	Gln Asp Phe Leu Phe Thr His Glu	
276	260	265	270
279 Cys	Glu Gln Ser Arg His Leu Asp	Leu Ala Val Gln Val Thr Glu Val	
280	275	280	285
283 Ile	Ala Tyr Thr His Cys Cys Val	Asn Pro Val Ile Tyr Ala Phe Val	
284	290	295	300
287 Gly	Glu Arg Phe Arg Lys Tyr Leu Arg	Gln Leu Phe His Arg Arg Val	
288 305		310	315 320
291 Ala	Val His Leu Val Lys Trp Leu Pro	Phe Leu Ser Val Asp Arg Leu	
292	325	330	335
295 Glu	Arg Val Ser Ser Thr Ser Pro	Ser Thr Gly Glu His Glu Leu Ser	
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299 Ala	Gly Phe		
300	355		
303 <210>	SEQ ID NO: 7		
304 <211>	LENGTH: 2156		
305 <212>	TYPE: DNA		
306 <213>	ORGANISM: Homo sapiens		
308 <400>	SEQUENCE: 7		
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313 atgcaactcc	gtgccagaag gtgaacgaga	gggccttttg ggcccaactg	ctgccccctc 180
315 tgtactcctt	ggtatttgtc attggcctgg	ttggaaacat cctggtggtc	ctggtccttg 240
317 tgcaatacaa	gaggctaaaa aacatgacca	gcatctacct cctgaacctg	gccatttctg 300
319 acctgctctt	cctggttcacg cttcccttct	ggatcgacta caagttgaag	gatgactggg 360
321 ttttttggtga	tgccatgtgt aagatcctct	ctgggtttta ttacacaggc	ttgtacagcg 420
323 agatcttttt	catcatcctg ctgacgattg	acaggtacct ggccatcgtc	cacgccgtgt 480
325 ttgccttgcg	ggcacggacc gtcacttttg	gtgtcatcac cagcatcatc	atttggggccc 540
327 tggccatctt	ggcttccatg ccaggcttat	acttttccaa gacccaatgg	gaattcactc 600
329 accacacctg	cagccttcac tttcctcacg	aaagcctacg agagtggaag	ctgtttcagg 660
331 ctctgaaact	gaacctcttt gggctggtat	tgcttttgtt ggtcatgac	atctgctaca 720
333 cagggattat	aaagattctg ctaagacgac	caaatgagaa gaaatccaaa	gctgtccgtt 780
335 tgatttttgt	catcatgac atcttttttc	tcttttggac cccctacaat	ttgactatac 840
337 ttatttctgt	tttccaagac ttctgtttca	cccatgagtg tgagcagagc	agacatttgg 900
339 acctggctgt	gcaagtgcag gaggtgatcg	cctacacgca ctgctgtgtc	aaccagtgga 960
341 tctacgcctt	cgttgggtgag aggttccgga	agtacctgcg gcagttgttc	cacaggcgtg 1020
343 tggctgtgca	cctgggttaaa tggctcccct	tcctctccgt ggacaggctg	gagaggggtca 1080
345 gctccacatc	tcctccaca ggggagcatg	aactctctgc tgggttctga	ctcagaccat 1140
347 aggaggccaa	cccaaaataa gcaggcgtga	cctgccaggc aactgagcc	agcagcctgg 1200
349 ctctcccagc	caggtttctga ctcttggcac	agcatggagt cacagccact	tgggatagag 1260
351 agggaatgta	atggtggcct ggggcttctg	aggcttctgg ggcttcagtc	ttttccatga 1320
353 acttctcccc	tggtagaaag aagatgaatg	agcaaaacca aatattccag	agactgggac 1380

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355 taagtgtacc agagaagggc ttggactcaa gcaagatttc agatttgtga ccattagcat 1440
357 ttgtcaacaa agtcacccac ttcccactat tgcttgcaaca aaccaattaa acccagtagt 1500
359 ggtgactgtg ggctccattc aaagtgaact cctaagccat gggagacact gatgtatgag 1560
361 gaatttctgt tcttccatca cctccccccc cccgccaccc tcccactgcc aagaacttgg 1620
363 aaatagtgat ttccacagtg actccactct gagtcccaga gccaatcagt agccagcatc 1680
365 tgctccccct tccactccac cgcaggattt gggctcttgg aatcctgggg aacatagaac 1740
367 tcatgacgga agagttgaga cctaacgaga aatagaaatg ggggaactac tgctggcagt 1800
369 ggaactaaga aagcccttag gaagaatttt tatatccact aaaatcaaac aattcaggga 1860
371 gtgggctaag cacgggccat atgaataaca tgggtgtgctt cttaaaatag ccataaaggg 1920
373 gagggactca tcatttccat ttacccttct tttctgacta tttttcagaa tctctcttct 1980
375 tttcaagttg ggtgatatgt tggtagattc taatggcttt attgcagcga ttaataacag 2040
377 gcaaaaggaa gcagggttgg tttcccttct ttttggtctt catctaagcc ttctggtttt 2100
379 atgggtcaga gttccgactg ccatcttggg cttgtcagca aaaaaaaaaa aaaaaa 2156
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383 <211> LENGTH: 355
384 <212> TYPE: PRT
385 <213> ORGANISM: Homo sapiens
387 <400> SEQUENCE: 8
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393 Asp Tyr Gly Asp Ala Thr Pro Cys Gln Lys Val Asn Glu Arg Ala Phe
394 20 25 30
397 Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Val Ile Gly
398 35 40 45
401 Leu Val Gly Asn Ile Leu Val Val Leu Val Leu Val Gln Tyr Lys Arg
402 50 55 60
405 Leu Lys Asn Met Thr Ser Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
406 65 70 75 80
409 Leu Leu Phe Leu Phe Thr Leu Pro Phe Trp Ile Asp Tyr Lys Leu Lys
410 85 90 95
413 Asp Asp Trp Val Phe Gly Asp Ala Met Cys Lys Ile Leu Ser Gly Phe
414 100 105 110
417 Tyr Tyr Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
418 115 120 125
421 Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala
422 130 135 140
425 Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Ile Ile Trp Ala Leu
426 145 150 155 160
429 Ala Ile Leu Ala Ser Met Pro Gly Leu Tyr Phe Ser Lys Thr Gln Trp
430 165 170 175
433 Glu Phe Thr His His Thr Cys Ser Leu His Phe Pro His Glu Ser Leu
434 180 185 190
437 Arg Glu Trp Lys Leu Phe Gln Ala Leu Lys Leu Asn Leu Phe Gly Leu
438 195 200 205
441 Val Leu Pro Leu Leu Val Met Ile Ile Cys Tyr Thr Gly Ile Ile Lys
442 210 215 220
445 Ile Leu Leu Arg Arg Pro Asn Glu Lys Lys Ser Lys Ala Val Arg Leu
446 225 230 235 240
449 Ile Phe Val Ile Met Ile Ile Phe Phe Leu Phe Trp Thr Pro Tyr Asn

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:48; N Pos. 5,6,7

Seq#:50; N Pos. 49

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:28,29

VERIFICATION SUMMARY

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L:573 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (15) SEQUENCE:

L:1781 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:0

L:1805 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:0